

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2003, 18:25:32 ; Search time 6.69697 Seconds
(without alignments)
91.287 Million cell updates/sec

Title: US-09-743-225-10
Perfect score: 66
Sequence: 1 CATLRVYKGGXA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	59.1	239	1 RPIA_CHLMU	Q9pk10 chlamydia m
2	38	57.6	405	1 PE21_MOUSE	P35375 mus musculus
3	38	57.6	6359	1 BACC_BACLI	O68008 b bacitraci
4	37	56.1	1435	1 TR85_HUMAN	Q9v215 homo sapien
5	36	54.5	367	1 INK4_DROME	Q9vrx6 drosophila
6	35	53.0	231	1 RPIA_AGRF5	Q8ue20 agrobacteri
7	35	53.0	231	1 RPIA_CHLPN	Q92942 chlamydia p
8	35	53.0	231	1 RPIA_RHIME	Q92pb8 rhizobium m
9	35	53.0	234	1 RPIA_METAC	O8tg69 methanosarc
10	35	53.0	242	1 RPIA_CHLTR	O84215 chlamydia t
11	35	53.0	244	1 PHOS_MOUSE	Q9gw08 mus musculus
12	35	53.0	245	1 PHOS_BOVIN	P15632 bos taurus
13	35	53.0	245	1 PHOS_FELCA	P41686 felis silve
14	35	53.0	246	1 PHOS_RAT	P20942 rattus norv
15	35	53.0	340	1 CFPA_BACUT	Q45729 bacillus th
16	35	53.0	424	1 VGLI_HSVB	P18553 equine herp
17	35	53.0	712	1 CDGT_BACS3	P09121 bacillus sp
18	35	53.0	713	1 AMYR_BACS8	P17692 bacillus sp
19	35	53.0	713	1 CDGT_BACSO	P05618 bacillus sp
20	35	53.0	713	1 CDGT_BACSP	P030921 bacillus sp
21	35	53.0	713	1 CDGU_BACCI	P43379 bacillus ci
22	34	51.5	110	1 THIO_STRCO	P52230 streptomyce
23	34	51.5	215	1 SC2_OCTDO	P27010 octopus dof
24	34	51.5	245	1 PHOS_CANPA	O77560 canis famli
25	34	51.5	246	1 PHOS_HUMAN	P20941 homo sapien
26	34	51.5	246	1 VMTV_LAMB	P03733 bacterioph
27	34	51.5	327	1 DRN1_STREQ	P26295 streptococc
28	34	51.5	345	1 APDH_HUMAN	P03749 homo sapien
29	34	51.5	349	1 ADH1_ASPTL	P41747 aspergillus
30	34	51.5	349	1 ADH1_EMENT	P08843 emericeila
31	34	51.5	349	1 RADA_PYRFO	O74036 pyrococcus
32	34	51.5	352	1 ADH3_EMENT	P07754 emericeila
33	34	51.5	353	1 ADH1_NEUCR	Q9p6c8 neurospora

34	34	51.5	356	1 RADA_PYRAB	Q9v233 pyrococcus
35	34	51.5	474	1 MPPA_BLAEM	P97997 blastoclad
36	34	51.5	529	1 RADA_PYRHO	O58001 pyrococcus
37	34	51.5	633	1 DXS_BACSU	P54523 bacillus su
38	34	51.5	637	1 PBPA_STORR	Q00573 streptococc
39	33	50.0	66	1 RS27_SULTO	Q973f9 sulfolobus
40	33	50.0	107	1 THIO_STRLC	Q05739 streptomyce
41	33	50.0	195	1 PYRE_SULSO	Q9ux09 sulfolobus
42	33	50.0	249	1 YAT6_RHOBL	P05449 rhodospseudo
43	33	50.0	270	1 URED_SYNF3	P73047 synecocyst
44	33	50.0	306	1 OPRR_PSEAE	Q01610 pseudomonas
45	33	50.0	340	1 ADHA_RHIME	O31186 rhizobium m

ALIGNMENTS

RESULT 1

ID	RPIA_CHLMU	STANDARD;	PRT;	239 AA.
AC	O9PK10;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)			
DE	(PRI).			
GN	RPIA OR TC0485.			
OS	Chlamydia muridarum.			
OC	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.			
OX	NCBI_TaxID=83560;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MoPn / Ni99;			
RX	MEDLINE=20150255; PubMed=10684935;			
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,			
RA	White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,			
RA	Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,			
RA	Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,			
RA	Eisen J., Fraser C.M.;			
RT	'Genome sequences of Chlamydia trachomatis MoPn and Chlamydia			
RT	pneumoniae AR39.';			
RL	Nucleic Acids Res. 28:1397-1406(2000).			
CC	-!- CATALYTIC ACTIVITY: D-ribose 5-phosphate - D-ribose 5-phosphate.			
CC	-!- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.			
CC	-!- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; AE002317; AAF39331.1; -			
DR	PIR; E81697; E81697.			
DR	TIGR; TC0485.			
DR	HAWAP; MF_00170; -; 1.			
DR	InterPro; IPR001034; HTH_Deor.			
DR	InterPro; IPR004788; Rpia.			
DR	Pfam; PF00455; Deor; 1.			
DR	ProDom; PD005813; Rpia; 1.			
KW	Isonerases; Complete proteome.			
SEQUENCE	239 AA; 26180 MW; CSAD6EAF682B3D37 CRC64;			

Query Match	59.1%;	Score 39;	DB 1;	Length 239;
Best Local Similarity	66.7%;	Pred No. 4.9;		
Matches	8;	Conservative	1;	Mismatches 3; Indels 0; Gaps 0;
QY	2	ATLRVYKGGXA 13		
DB	102	ANLRWKGCGGA 113		

RESULT 2

PE21 MOUSE STANDARD; PRT; 405 AA.

AC P35375.

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE prostaglandin E2 receptor, EPI subtype (prostanoid EPI receptor) (PGE receptor, EPI subtype).

GN PTGER1 OR PTGEREPI.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ddy; TISSUE=Kidney;

RX MEDLINE=9338584; PubMed=7690750;

RA Watabe A., Sugimoto Y., Honda A., Irie A., Namba T., Negishi M., Ito S., Narumiya S., Ichikawa A.;

RT "Cloning and expression of cDNA for a mouse EPI subtype of prostaglandin E receptor".

RT J. Biol. Chem. 268:20175-20178(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129;

RX MEDLINE=95377316; PubMed=7649181;

RA Batschke B., Nilsson C., Sundelin J.;

RT "Molecular characterization of the mouse prostanoid EPI receptor gene".

RT Eur. J. Biochem. 231:809-814(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129;

RX MEDLINE=97011095; PubMed=8858105;

RA Batschke B., Sundelin S.;

RT "The mouse genes for the EPI prostanoid receptor and the PKN protein kinase overlap".

RT Biochem. Biophys. Res. Commun. 227:70-76(1996).

CC -!- FUNCTION: RECEPTOR FOR PROSTAGLANDIN E2 (PGE2). THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-Q PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. MAY PLAY A ROLE AS AN IMPORTANT MODULATOR OF RENAL FUNCTION. IMPLICATED THE SMOOTH MUSCLE CONTRACTILE RESPONSE TO PGE2 IN VARIOUS TISSUES.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: ABUNDANT IN KIDNEY AND IN A LESSER AMOUNT IN LUNG.

CC -!- PTM: PHOSPHORYLATED (POTENTIAL).

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL: D16338; BAA03842.1; -

DR EMBL: Z45987; CAA90278.1; -

DR EMBL: Y07611; CAA68884.1; -

DR PIR: S66525; S66525.

DR MGD: MGI:97793; Ptger1.

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PROSITE: PS00437; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE: PS00362; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation.

FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 40 62 1 (POTENTIAL).

FT DOMAIN 63 80 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 81 99 2 (POTENTIAL).

FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 114 135 3 (POTENTIAL).

FT DOMAIN 136 157 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 158 179 4 (POTENTIAL).

FT DOMAIN 180 202 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 203 228 5 (POTENTIAL).

FT DOMAIN 229 301 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 302 323 6 (POTENTIAL).

FT DOMAIN 324 337 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 338 357 7 (POTENTIAL).

FT DOMAIN 358 405 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 7 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 24 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 34 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 112 190 BY SIMILARITY.

SQ SEQUENCE 405 AA; 42965 MW; 2564DA21005CF8D6 CRC64;

Query Match 57.6%; Score 38; DB 1; Length 405;

Best Local Similarity 66.7%; Pred. No. 13;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATLRYVKGXGA 13

DB 277 ATLRSSRGSSA 288

RESULT 3

BACC_BACLI STANDARD; PRT; 6359 AA.

ID BACC_BACLI

AC 068008;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bacitracin synthetase 3 (BA3) [Includes: ATP-dependent isoleucine adenylation (IleA) (isoleucine activase); ATP-dependent D-phenylalanine adenylation (D-PheA) (D-phenylalanine activase); ATP-dependent histidine adenylation (HisA) (histidine activase); ATP-dependent D-aspartate adenylation (D-AspA) (D-aspartate activase); ATP-dependent asparagine adenylation (AsnA) (asparagine activase); Aspartate racemase (EC 5.1.1.13); Phenylalanine racemase [ATP hydrolyzing] (EC 5.1.1.11)].

GN BACC.

OS Bacillus licheniformis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1402;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 10716;

RX MEDLINE=98089193; PubMed=9427658;

RA Konz D., Klenz A., Schoergendorfer K., Marahiel M.A.;

RT "The bacitracin biosynthesis operon of Bacillus licheniformis ATCC 10716: molecular characterization of three multi-modular peptide synthetases".

RL Chem. Biol. 4:927-937(1997).

CC -!- FUNCTION: INDUCES PEPTIDE SYNTHESIS, ACTIVATES AND INCORPORATES FIVE AMINO ACIDS, FORMS A THIAZOLINE RING BETWEEN THE FIRST TWO AMINO ACIDS AND INCORPORATES A D-GLUTAMINE IN THE FOURTH POSITION.

CC -!- CATALYTIC ACTIVITY: L-aspartate -> D-aspartate.

CC -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine -> AMP + diphosphate + D-phenylalanine.

CC -!- COFACTOR: CONTAINS 5 COVALENTLY BOUND PHOSPHOPANTHETINES (POTENTIAL).

CC -!- PATHWAY: Cyclic peptide antibiotic bacitracin biosynthesis.

CC -!- SUBUNIT: LARGE MULTIMERIC COMPLEX OF BA1, BA2 AND BA3.

CC -!- DOMAIN: CONSISTS OF FIVE MODULES WITH TWO EPIMERIZATION DOMAINS IN THE SECOND AND FOURTH MODULES, AND A PUTATIVE C-TERMINAL THIOESTERASE DOMAIN. EACH MODULE INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOLATION, CONDENSATION (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL), AND N METHYLATION (OPTIONAL).

CC -!- MISCELLANEOUS: BACITRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
OX [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC
RC TISSUE=Brain;
RX MEDLINE=994246063; PubMed=10231032;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RT Genome Res. 6:63-70(1999).
RL [2]
RL SEQUENCE FROM N.A. (ISOFORM 2).
RC
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166;
RA Wlemann S., Weil B., Wellenreuther R., Gassenhüber J., Glassl S.,
RA Ansong W., Boscher M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
RA Meves H.-W., Ottenwaelter B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RA "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RT Genome Res. 11:422-435(2001).
RL [3]
RL IDENTIFICATION IN TRAPP COMPLEX.
RX MEDLINE=21664186; PubMed=11805826;
RA Gavin A.C., Bosche M., Krause R., Grandi P., Marzioch M., Bauer A.,
RA Schultz J., Rick J.M., Michon A.M., Cruciati C.M., Remor M., Hofert C.,
RA Scheider M., Brajenovic M., Rufiner H., Merino K., Klein K., Hudak M.,
RA Dickson D., Rudi T., Gnau V., Bauch A., Bastuck S., Huhse B.,
RA Leutwein C., Heurlier M.A., Copley R.R., Edelmann A., Querfurth E.,
RA Rybin V., Drewes G., Raide M., Boumeester T., Bork P., Seraphin B.,
RA Kuster B., Neubauer G., Superti-Furga G.;
RA "Functional organization of the yeast proteome by systematic analysis
RT of protein complexes.";
RT Nature 415:141-147(2002).
RL -1- FUNCTION: May play role in vesicular transport from endoplasmic
RL reticulum to Golgi.
CC -1- SUBUNIT: Part of the multisubunit TRAPP (transport protein
CC complex.
CC -1- SUBCELLULAR LOCATION: Cis-Golgi complex (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Y2L5-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9Y2L5-2; Sequence=VSP_004000;
CC Note=No experimental confirmation available;
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB023229; BAA76856.1; -
CC EMBL; AL136749; CAB66683.1; -
DR GO: GO:0005801; C:Golgi cis-face; NAS.
DR GO: GO:0005478; F:Intracellular transporter activity; NAS.
DR GO: GO:0006888; P:ER to Golgi transport; NAS.
KW transport; Endoplasmic reticulum; Golgi stack; Alternative splicing.
FT VARSPLIT 916 1002 Missing (in isoform 2).
FT /FTID=VSP_004000.
FT CONFLICT 251 251 K -> E (IN REF. 2).
FT CONFLICT 1146 1146 A -> T (IN REF. 2).
SQ SEQUENCE 1435 AA; 160940 MW; 35C7C965CE422B04 CRC64;
Query Match 56.1%; Score 37; DB 1; Length 1435;

Best Local Similarity 54.5%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 0; Gaps 0;

QY 1 CATLRVYKGG 11
Db 585 COAMQVYKGG 595

RESULT 5
INX4_DROME
ID INX4_DROME STANDARD; PRT; 367 AA.
AC Q9VRX6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE InneXin INX4 (InneXin-4) (zero population growth protein).
GN ZPG OR INX4 OR CG10125.
OS Drosophila melanogaster. (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE-Ovary;
RX MEDLINE=21959302; PubMed=11960713;
RA Stebbings L.A., Todman M.G., Phillips R., Greer C.E., Tam J.,
RA Phelan P., Jacobs K., Bacon J.P., Davies J.A.;
RT "Gap junctions in Drosophila: developmental expression of the entire
RT InneXin gene family.";
RL Mech. Dev. 113:197-205 (2002).
RN [2]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC TISSUE-Ovary;
RX PubMed=11973283;
RA Tazuke S.I., Schulz C., Gilboa L., Fogarty M., Mahowald A.P.,
RA Guichet A., Ephrussi A., Wood C.G., Lehmann R., Fuller M.T.;
RT "A germline-specific gap junction protein required for survival of
RT differentiating early germ cells.";
RL Development 129:2529-2539 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Foster C., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Embryo;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Kronmiller B., Pacle J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
CC -!- FUNCTION: Structural component of the gap junctions in germ line
CC cells. Required for differentiation and survival of germline cysts
CC in females and of spermatogonia in males; gap junctional
CC communication between spermatogonia and somatic cyst cells may be
CC required for normal differentiation and survival of spermatogonia.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein; concentrated at
CC the interface between germline and somatic support cells in
CC spermatogonia, early spermatocytes and germ cells in the ovary.
CC -!- TISSUE SPECIFICITY: Expressed in nurse cells and oocyte during
CC oogenesis. Uniform expression in imaginal wing disk and low
CC expression in developing imaginal CNS. Expressed in embryonic pole
CC cells and primordial germ cells.
CC -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
CC First seen at the embryonic syncytial blastoderm stage.
CC -!- SIMILARITY: Belongs to the innexin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF271718; AAL36976.1; -
CC EMBL: AF003562; AAF50655.1; -
CC EMBL: AY094856; AAM11209.1; -
CC FlyBase: FBgn024177; zpg.
CC GO: GO:0007281; P:germ-cell development; IMP.
CC InterPro: IPR000990; Innexin.
CC Pfam: PF00876; Innexin; 1.
CC PRINTS: PR01262; INNEXIN.
KW Gap junction; Transmembrane.
FT DOMAIN 1 21
FT TRANSMEM 22 42 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 110 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 111 131 POTENTIAL.
FT DOMAIN 132 186 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 187 207 POTENTIAL.
FT DOMAIN 208 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 289 POTENTIAL.
FT DOMAIN 290 367 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 367 AA; 42784 MW; B984A4035DA7CF3E CRC64;

Query Match 54.5%; Score 36; DB 1; Length 367;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATLRVYKGG 10
Db 237 CAKCEMIRGG 246

RESULT 6

```

RPIA_AGR5S
ID RPIA_AGR5S STANDARD; PRT; 231 AA.
AC Q92942; Q9JQ38;
DT 15-SEP-2003 (Rel. 42, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
DE (PRI).
DE RPIA OR ATU1613 OR AGR_C-2972.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Senphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Foo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RT Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao X., Astensari M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA William C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RT Science 294:2323-2328(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RT Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWI029 from USA."
RT Nucleic Acids Res. 28:2311-2314(2000).
CC -1- CATALYTIC ACTIVITY: D-ribose 5-phosphate - D-ribose 5-phosphate.
CC -1- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
CC -1- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001600; AAF18294.1; -
DR EMBL; AE002221; AAF38446.1; -
DR EMBL; AF002545; BAA98351.1; -
DR PIR; B72115; B72115.
DR PIR; E86508; E86508.
DR TIGR; CP0631; -
DR HAMAP; MF_00170; -; 1.
DR InterPro; IPR004788; RPIA.
DR ProDom; PD005813; RPIA; 1.
KW Isomerase; Complete proteome.
SQ SEQUENCE 231 AA; 25574 MW; C2DD9CFF6F370C17 CRC64;
Query Match 53.0%; Score 35; DB 1; Length 231;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 LRVYKGGGXA 13
||: |||||
DB 92 LRLVKGGGGA 101

```

```

Db      96 LRMIKGGGA 105

RESULT 8
RPIA_RHIME
ID RPIA_RHIME STANDARD; PRT; 231 AA.
AC Q92PB8;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
DE (PRI).
GN RPIA OR R01856 OR SMC00152.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Bostard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT 'Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.';
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -|- CATALYTIC ACTIVITY: D-ribose 5-phosphate -> D-ribulose 5-phosphate.
CC -|- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
CC -|- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL591788; CAC46435.1; -.
DR HAMAP; MF_00170; -.
DR InterPro; IPR001034; HTH_Deor.
DR InterPro; IPR004788; RpiA.
DR Pfam; PF00455; deor; 1.
DR ProDom; PD005813; RpiA; 1.
DR TIGRFAMs; TIGR00021; rpiA; 1.
KW Isomerase; Complete proteome.
SQ SEQUENCE 231 AA; 24054 MW; 461B9638D4E9C448 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 231;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 LRVYKGGGA 13
DB 92 LRLKGGGA 101
||:|||||

RESULT 9
RPIA_METAC
ID RPIA_METAC STANDARD; PRT; 234 AA.
AC Q8TQ69;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
DE (PRI).
GN RPIA OR M1683.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.

OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
CC -|- CATALYTIC ACTIVITY: D-ribose 5-phosphate -> D-ribulose 5-phosphate.
CC -|- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
CC -|- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE010842; AM05090.1; -.
DR HAMAP; MF_00170; -.
DR InterPro; IPR004788; RpiA.
DR ProDom; PD005813; RpiA; 1.
DR TIGRFAMs; TIGR00021; rpiA; 1.
KW Isomerase; Complete proteome.
SQ SEQUENCE 234 AA; 24940 MW; 7CCDD8FE179FE5D0 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 234;
Best Local Similarity 70.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 LRVYKGGGA 13
DB 99 LRAIKGGGA 108
||:|||||

RESULT 10
RPIA_CHLTR
ID RPIA_CHLTR STANDARD; PRT; 242 AA.
AC O84215;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
DE (PRI).
GN RPIA OR CT213.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -|- CATALYTIC ACTIVITY: D-ribose 5-phosphate -> D-ribulose 5-phosphate.
CC -|- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.

```

CC -1- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF001295; AAC67805.1; -
 CC PIR; D71542; D71542.
 CC HAMAP; MF-00170; -; 1.
 CC InterPro; IPR001034; HTH_Deor.
 CC InterPro; IPR004788; RpiA.
 CC Pfam; PF00455; deor; 1.
 CC ProDom; PD005813; RpiA; 1.
 CC Isomerase; Complete proteome.
 CC SEQUENCE 242 AA; 26646 MW; D59C38284D2229B2 CRC64;
 CC
 CC Query Match 53.0%; Score 35; DB 1; Length 242;
 CC Best Local Similarity 70.0%; Pred. No. 28;
 CC Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC QY 4 LRVYKGGXA 13
 CC ||: |||||
 CC DB 104 LRVYKGGGA 113
 CC
 CC RESULT 11
 CC PHOS_MOUSE
 CC ID PHOS_MOUSE STANDARD; PRT; 244 AA.
 CC AC Q9QW08;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Phosducin (PHD) (33 kDa phototransducing protein) (Rod photoreceptor
 CC DE 1) (RPR-1).
 CC DE PDC OR RPRI.
 CC GN Mus musculus (Mouse).
 CC OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=BALE/c; TISSUE=Retina;
 CC RX MEDLINE=94009395; PubMed=8405193;
 CC RA Groszhan K.R., Norton J.C., Craft C.M., Travis G.H.;
 CC RT "Isolation and characterization of a cDNA for mouse retinal
 CC RT phosducin".
 CC RL Exp. Eye Res. 57:253-255(1993).
 CC CC -1- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
 CC CC PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
 CC CC METABOLISM.
 CC CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of
 CC CC the GTP-binding protein, transducin.
 CC CC -1- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
 CC CC -1- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
 CC CC MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
 CC CC -1- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L08075; AAK13559.1; -
 CC PIR; JC2018; JC2018.
 CC HSP; P20942; IB9X.
 CC MGD; MGI:98090; Pdc.
 CC

DR InterPro; IPR001200; Phosducin.
 DR InterPro; IPR006663; Thioresox_dom2.
 DR Pfam; PF02114; Phosducin; 1.
 DR PRINTS; P00677; PHOSDUCIN.
 KW Vision; Sensory transduction; Phosphorylation.
 CC MOD_RES 71 71 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 CC SEQUENCE 244 AA; 28016 MW; F42361EA25F0F254 CRC64;
 CC
 CC Query Match 53.0%; Score 35; DB 1; Length 244;
 CC Best Local Similarity 87.5%; Pred. No. 28;
 CC Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 3 TLRVYKGG 10
 CC ||: |||||
 CC DB 186 TLRVYKGG 193
 CC
 CC RESULT 12
 CC PHOS_BOVIN
 CC ID PHOS_BOVIN STANDARD; PRT; 245 AA.
 CC AC P19632; P20940; Q28160;
 CC DT 01-FEB-1991 (Rel. 17, Created)
 CC DT 01-MAY-1991 (Rel. 18, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Phosducin (PHD) (33 kDa phototransducing protein) (MEKA protein).
 CC GN PDC.
 CC OS Bos taurus (Bovine).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Bovinae; Bos.
 CC OX NCBI_TaxID=9913;
 CC RN [1]
 CC RP SEQUENCE, AND SEQUENCE OF 228-245 FROM N.A.
 CC RC TISSUE=Retina;
 CC RX MEDLINE=90368806; PubMed=2203790;
 CC RA Lee R.H., Fowler A., McGinnis J.F., Lolley R.N., Craft C.M.;
 CC RT "Amino acid and cDNA sequence of bovine phosducin, a soluble
 CC RT phosphoprotein from photoreceptor cells".
 CC RL J. Biol. Chem. 265:15867-15873(1990).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=89364083; PubMed=2770450;
 CC RA Kuo C.-H., Akiyama M., Miki N.;
 CC RT "Isolation of a novel retina-specific clone (MEKA cDNA) encoding a
 CC RT photoreceptor soluble protein".
 CC RL Brain Res. Mol. Brain Res. 6:1-10(1989).
 CC RN [3]
 CC RP SEQUENCE OF 8-245 FROM N.A.
 CC RC TISSUE=Pinel gland, and Retina;
 CC RX MEDLINE=91007277; PubMed=2210381;
 CC RA Abe T., Nakabayashi H., Tamada H., Takagi T., Sakuragi S., Yamaki K.,
 CC RA Shinohara T.;
 CC RT "Analysis of the human, bovine and rat 33-kDa proteins and cDNA in
 CC RT retina and pineal gland".
 CC RL Gene 91:209-215(1990).
 CC RN [4]
 CC RP PHOSPHORYLATION OF SER-73.
 CC RX MEDLINE=90368805; PubMed=2394752;
 CC RA Lee R.H., Brown B.M., Lolley R.N.;
 CC RT "Protein kinase A phosphorylates retinal phosducin on serine 73 in
 CC RT situ".
 CC RL J. Biol. Chem. 265:15860-15866(1990).
 CC RN [5]
 CC RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH G-BETA AND
 CC RP G-GAMMA.
 CC RX MEDLINE=98416696; PubMed=9739091;
 CC RA Loew A., Ho Y.K., Blundell T., Bax B.;
 CC RT "Phosducin induces a structural change in transducin beta gamma".
 CC RL Structure 6:1007-1019(1998).
 CC CC -1- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
 CC CC PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
 CC CC METABOLISM.
 CC CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of

the GTP-binding protein, transducin.
 -|- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.
 -|- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS
 MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.
 -|- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
 -|- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINUS
 DUE TO A FRAMESHIFT.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 EMBL; M58170; AAA62116.1; -
 EMBL; M33529; AAA30349.1; -
 PIR; A38379; A38379.
 PDB; 1A0R; 16-FEB-99.
 InterPro; IPR001200; Phosducin.
 InterPro; IPR006663; Thioresox_dom2.
 Pfam; PF02114; Phosducin; 1.
 PRINTS; PR00677; PHOSDUCIN.
 Vision; Sensory transduction; Phosphorylation; 3D-structure.
 MOD_RES 73 73 PHOSPHORYLATION (BY PKA).
 CONFLICT 44 44 H -> P (IN REF. 3).
 CONFLICT 238 239 TN -> SK (IN REF. 3).
 HELIX 21 35
 TURN 36 36
 HELIX 74 80
 TURN 81 82
 HELIX 87 105
 STRAND 114 116
 HELIX 120 128
 TURN 132 133
 STRAND 135 141
 TURN 143 144
 TURN 146 147
 HELIX 148 161
 TURN 163 164
 STRAND 166 171
 HELIX 172 175
 TURN 178 179
 TURN 183 185
 STRAND 188 193
 TURN 194 195
 STRAND 196 201
 TURN 202 203
 HELIX 204 207
 TURN 210 211
 HELIX 214 222
 TURN 223 225
 SEQUENCE 245 AA; 28231 MW; 5CA621610401D550 CRC64;
 Query Match 53.0%; Score 35; DB 1; Length 245;
 Best Local Similarity 87.5%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TLRYKGG 10
 || |||||
 Db 188 TLLYKGG 195

RESULT 13
 PHOS_FELCA
 ID PHOS_FELCA STANDARD; PRT; 245 AA.
 AC P41686;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosducin (PHD) (33 kDa phototransducing protein).
 GN PDC.

OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Abysinnian; TISSUE=Retina;
 RX MEDLINE=95178554; PubMed=7873608;
 RA Gorin M.B., To A.C., Narfstrom K.;
 RT "Sequence analysis and exclusion of phosducin as the gene for the
 recessive retinal degeneration of the Abyssinian cat.";
 RL Biochim. Biophys. Acta 1260:323-327(1995).
 CC -|- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
 PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
 METABOLISM.
 CC -|- SUBUNIT: Forms a complex with the beta and gamma subunits of
 the GTP-binding protein, transducin.
 CC -|- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS
 (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 EMBL; L35314; AAB59257.1; -
 PIR; S52096; S52096.
 HSP; P20942; 1B9X.
 InterPro; IPR001200; Phosducin.
 InterPro; IPR006663; Thioresox_dom2.
 Pfam; PF02114; Phosducin; 1.
 PRINTS; PR00677; PHOSDUCIN.
 Vision; Sensory transduction; Phosphorylation.
 MOD_RES 73 73 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 SEQUENCE 245 AA; 28363 MW; 9807CD30C32F8B21 CRC64;
 Query Match 53.0%; Score 35; DB 1; Length 245;
 Best Local Similarity 87.5%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TLRYKGG 10
 || |||||
 Db 188 TLLYKGG 195

RESULT 14
 PHOS_RAT
 ID PHOS_RAT STANDARD; PRT; 246 AA.
 AC P20942; Q63420;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Phosducin (PHD) (33 kDa phototransducing protein) (MEKA protein) (Rod
 photoreceptor 1) (RPR-1).
 GN PDC OR RPRI.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Pineal gland, and Retina;
 RX MEDLINE=9100727; PubMed=2210381;
 RA Abe T., Nakabayashi H., Tamada H., Takagi T., Sakuragi S., Yamaki K.,
 RA Shinohara T.;
 RT "Analysis of the human, bovine and rat 33-kDa proteins and cDNA in
 retina and pineal gland.";
 RL Gene 91:209-215(1990).
 RN [2]


```

TURN 202 203
HELIX 204 207
HELIX 214 222
TURN 223 225
SEQUENCE 246 AA; 28129 MW; 3C48ABC84E5E3D04 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 246;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TLRVYKGG 10
|||
188 TLLVYKGG 195

-----
CFPAA_BACUT STANDARD; PRT; 340 AA.
Q45729;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidal crystal protein cry15a (insecticidal delta-endotoxin
CRYXA(A)) (Crystalline entomocidal protoxin) (38 kDa crystal
protein).
CRY15AA OR CRYXA(A).
Bacillus thuringiensis (subsp. thompsoni).
Plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=44162;
[1]
SEQUENCE FROM N.A.
MEDLINE=92105024; PubMed=1729243;
Brown K.L., Whiteley H.R.;
"Molecular characterization of two novel crystal protein genes from
Bacillus thuringiensis subsp. thompsoni.";
J. Bacteriol. 174:549-557(1992).
-|- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE.
-|- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announcement/
or send an email to license@isb-sib.ch).
-----
EMBL; M76442; AAA22333.1; -
PIR; B41969; B41969.
InterPro; IPR005831; Aer_hem.
Toxin; Sporulation; Plasmid.
SEQUENCE 340 AA; 37547 MW; BCBFA24FE9B1FA50 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 340;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATLRYVKG 9
|||
160 ATLQYVKG 167

-----
CFPAA_BACUT STANDARD; PRT; 340 AA.
Q45729;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidal crystal protein cry15a (insecticidal delta-endotoxin
CRYXA(A)) (Crystalline entomocidal protoxin) (38 kDa crystal
protein).
CRY15AA OR CRYXA(A).
Bacillus thuringiensis (subsp. thompsoni).
Plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=44162;
[1]
SEQUENCE FROM N.A.
MEDLINE=92105024; PubMed=1729243;
Brown K.L., Whiteley H.R.;
"Molecular characterization of two novel crystal protein genes from
Bacillus thuringiensis subsp. thompsoni.";
J. Bacteriol. 174:549-557(1992).
-|- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE.
-|- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announcement/
or send an email to license@isb-sib.ch).
-----
EMBL; M76442; AAA22333.1; -
PIR; B41969; B41969.
InterPro; IPR005831; Aer_hem.
Toxin; Sporulation; Plasmid.
SEQUENCE 340 AA; 37547 MW; BCBFA24FE9B1FA50 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 340;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATLRYVKG 9
|||
160 ATLQYVKG 167

-----
CFPAA_BACUT STANDARD; PRT; 340 AA.
Q45729;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidal crystal protein cry15a (insecticidal delta-endotoxin
CRYXA(A)) (Crystalline entomocidal protoxin) (38 kDa crystal
protein).
CRY15AA OR CRYXA(A).
Bacillus thuringiensis (subsp. thompsoni).
Plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=44162;
[1]
SEQUENCE FROM N.A.
MEDLINE=92105024; PubMed=1729243;
Brown K.L., Whiteley H.R.;
"Molecular characterization of two novel crystal protein genes from
Bacillus thuringiensis subsp. thompsoni.";
J. Bacteriol. 174:549-557(1992).
-|- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE.
-|- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announcement/
or send an email to license@isb-sib.ch).
-----
EMBL; M76442; AAA22333.1; -
PIR; B41969; B41969.
InterPro; IPR005831; Aer_hem.
Toxin; Sporulation; Plasmid.
SEQUENCE 340 AA; 37547 MW; BCBFA24FE9B1FA50 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 340;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATLRYVKG 9
|||
160 ATLQYVKG 167

-----
CFPAA_BACUT STANDARD; PRT; 340 AA.
Q45729;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidal crystal protein cry15a (insecticidal delta-endotoxin
CRYXA(A)) (Crystalline entomocidal protoxin) (38 kDa crystal
protein).
CRY15AA OR CRYXA(A).
Bacillus thuringiensis (subsp. thompsoni).
Plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=44162;
[1]
SEQUENCE FROM N.A.
MEDLINE=92105024; PubMed=1729243;
Brown K.L., Whiteley H.R.;
"Molecular characterization of two novel crystal protein genes from
Bacillus thuringiensis subsp. thompsoni.";
J. Bacteriol. 174:549-557(1992).
-|- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE.
-|- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announcement/
or send an email to license@isb-sib.ch).
-----
EMBL; M76442; AAA22333.1; -
PIR; B41969; B41969.
InterPro; IPR005831; Aer_hem.
Toxin; Sporulation; Plasmid.
SEQUENCE 340 AA; 37547 MW; BCBFA24FE9B1FA50 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 340;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATLRYVKG 9
|||
160 ATLQYVKG 167

-----
CFPAA_BACUT STANDARD; PRT; 340 AA.
Q45729;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidal crystal protein cry15a (insecticidal delta-endotoxin
CRYXA(A)) (Crystalline entomocidal protoxin) (38 kDa crystal
protein).
CRY15AA OR CRYXA(A).
Bacillus thuringiensis (subsp. thompsoni).
Plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=44162;
[1]
SEQUENCE FROM N.A.
MEDLINE=92105024; PubMed=1729243;
Brown K.L., Whiteley H.R.;
"Molecular characterization of two novel crystal protein genes from
Bacillus thuringiensis subsp. thompsoni.";
J. Bacteriol. 174:549-557(1992).
-|- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE.
-|- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announcement/
or send an email to license@isb-sib.ch).
-----
EMBL; M76442; AAA22333.1; -
PIR; B41969; B41969.
InterPro; IPR005831; Aer_hem.
Toxin; Sporulation; Plasmid.
SEQUENCE 340 AA; 37547 MW; BCBFA24FE9B1FA50 CRC64;

Query Match 53.0%; Score 35; DB 1; Length 340;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATLRYVKG 9
|||
160 ATLQYVKG 167

-----
CFPAA_BACUT STANDARD; PRT; 340 AA.
Q45729;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidal crystal protein cry15a (insecticidal delta-endotoxin
CRYXA(A)) (Crystalline entomocidal protoxin) (38 kDa crystal
protein).
CRY15AA OR CRYXA(A).
Bacillus thuringiensis (subsp. thompsoni).
Plasmid.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=44162;
[1]
SEQUENCE FROM N.A.
MEDLINE=92105024; PubMed=1729243;
Brown K.L., Whiteley H.R.;
"Molecular characterization of two novel crystal protein genes from
Bacillus thuringiensis subsp. thompsoni.";
J. Bacteriol. 174:
```